

Cunningham 3968
RAW SEQUENCE LISTING
PATENT APPLICATION US/08/819,669

1816

DATE: 10/14/97
TIME: 16:34:31

INPUT SET: S20989.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
Lurquin, Christophe; Chomez, Patrick; Traversari, Catia

(ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
Rejection Antigens and Uses Thereof

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Felfe & Lynch
(B) STREET: 805 Third Avenue
(C) CITY: New York City
(D) STATE: New York
(F) ZIP: 10022

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
(B) COMPUTER: IBM
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/819,669
(B) FILING DATE: 17-MAR-1997
(C) CLASSIFICATION: 530

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/142,368
(B) FILING DATE: 02-MAY-1994

(A) APPLICATION NUMBER: PCT/US92/04354
(B) FILING DATE: 22-MAY-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/807,043
(B) FILING DATE: 12-DECEMBER-1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/764,364
(B) FILING DATE: 23-SEPTEMBER-1991

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PATENT APPLICATION US/08/819,669DATE: 10/14/97
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47 (vii) PRIOR APPLICATION DATA:
48 (A) APPLICATION NUMBER: 07/728,838
49 (B) FILING DATE: 9-JULY-1991
50
51 (vii) PRIOR APPLICATION DATA:
52 (A) APPLICATION NUMBER: 07/705,702
53 (B) FILING DATE: 23-May-1991
54
55 (viii) ATTORNEY/AGENT INFORMATION:
56 (A) NAME: Hanson, Norman D.
57 (B) REGISTRATION NUMBER: 30,946
58 (C) REFERENCE/DOCKET NUMBER: LUD 5253.4-US
59
60 (ix) TELECOMMUNICATION INFORMATION:
61 (A) TELEPHONE: (212) 688-9200
62 (B) TELEFAX: (212) 838-3884
63
64
65

66 (2) INFORMATION FOR SEQ ID NO: 1:
67 (i) SEQUENCE CHARACTERISTICS:
68 (A) LENGTH: 462 base pairs
69 (B) TYPE: nucleic acid
70 (C) STRANDEDNESS: single
71 (D) TOPOLOGY: linear
72 (ii) MOLECULE TYPE: genomic DNA
73 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
74
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78	ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG	60
79	ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT	120
80	CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTGTGCA AGTTCCGCCT ACAGCTCTAG	180
81	CTTGTGAATT TGTACCCCTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC	240
82	CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
83	AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG CATGCATTGT	360
84	GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT	420
85	TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC	462

86
87
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90 (2) INFORMATION FOR SEQ ID NO: 2:
91 (i) SEQUENCE CHARACTERISTICS:
92 (A) LENGTH: 675 base pairs
93 (B) TYPE: nucleic acid
94 (C) STRANDEDNESS: single
95 (D) TOPOLOGY: linear
96 (ii) MOLECULE TYPE: genomic DNA
97 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
98
99

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100	ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT	48
101	Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly	
102	5 10 15	
103	GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA	96
104	Asp Gly Asp Gly Asn Arg Cys Asn Leu His Arg Tyr Ser Leu Glu	
105	20 25 30	
106	GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA	144
107	Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr	
108	35 40 45	
109	AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG	192
110	Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln	
111	50 55 60	
112	TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC	240
113	Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser	
114	65 70 75 80	
115	TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC	288
116	Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr	
117	85 90 95	
118	GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	336
119	Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp	
120	100 105 110	
121	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG	384
122	Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu	
123	115 120 125	
124	GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG	432
125	Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met	
126	130 135 140	
127	GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG	480
128	Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys	
129	145 150 155 160	
130	AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC	528
131	Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe	
132	165 170 175	
133	CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT	576
134	Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys	
135	180 185 190	
136	GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG	624
137	Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu	
138	195 200 210	
139	GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	672
140	Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro	
141	220 225 230 235	
142		
143	TAG	675
144		
145		
146		

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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153 (ii) MOLECULE TYPE: genomic DNA
154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
155
156
157
158 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT 60
159 TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT 120
160 TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACCTT CATATGATAC 180
161 ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC 228
162
163

164 (2) INFORMATION FOR SEQ ID NO: 4:
165 (i) SEQUENCE CHARACTERISTICS:
166 (A) LENGTH: 1365 base pairs
167 (B) TYPE: nucleic acid
168 (C) STRANDEDNESS: single
169 (D) TOPOLOGY: linear
170 (ii) MOLECULE TYPE: genomic DNA
171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
172
173

174 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50
175 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100
176 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
177 AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200
178 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
179 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
180 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG 350
181 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
182 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
183 ACCCTTTGTG CC 462
184 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
185 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
186 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
187 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
188 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
189 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
190 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
191 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
192 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
193 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
194 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC GTT CCT 924
195 GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966
196 TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008
197 AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050
198 GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092
199 GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 1134
200 TAG 1137
201 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG 1187
202 TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA 1237
203 ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT 1287
204 CTGACTGCAT GGTGAACCTT CATATGATAC ATAGGATTAC ACTTGTACCT 1337
205 GTTAAAAATA AAAGTTTGAC TTGCATAC 1365

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209 (2) INFORMATION FOR SEQ ID NO: 5:

210 (i) SEQUENCE CHARACTERISTICS:

211 (A) LENGTH: 4698 base pairs

212 (B) TYPE: nucleic acid

213 (C) STRANDEDNESS: single

214 (D) TOPOLOGY: linear

215 (ii) MOLECULE TYPE: genomic DNA

216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

217

218	ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
219	GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT	100
220	CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG	150
221	AAGTTTTGCA AGTTCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT	200
222	CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA	250
223	CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
224	AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG	350
225	CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG	400
226	CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
227	ACCCTTTGTG CC	462
228	ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
229	GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
230	TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
231	TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
232	ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
233	TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
234	GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC	756
235	GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
236	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
237	GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
238	GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T	916
239	GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA	966
240	CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC	1016
241	TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC	1066
242	CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC	1116
243	TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC	1166
244	TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCCTC	1216
245	TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCCCTCCC TTCTGTGTTCC	1266
246	CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT	1316
247	TCACCAGCTT TGCTCTCCCT GCTCCCTCC CCCTTTTGCA CCTTTTCTTT	1366
248	TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT	1416
249	CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG	1466
250	TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT	1516
251	CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT	1566
252	TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCTGGCAC	1616
253	TCACTCTGTA GACCAGGCTG GCCTCAAAC CAGAAATCTG CCTGCCTCTG	1666
254	CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG	1716
255	GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT	1766
256	AACTCCCTTT TTGGCACCTT TCCTTTACAG GACCCCTCC CCTCCCTGT	1816
257	TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC	1866
258	CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTGCTTTCT	1916

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